

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

EFS

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/578,839A
Source: IFW
Date Processed by STIC: 2/26/07

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/578,839A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line **not exceed** 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.

- 4 Non-ASCII The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for **each** skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped
 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If **intentional**, please insert the following lines for **each** skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.
 In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.

- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. **Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."**
 Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 Misuse of n/Xaa "**n**" can **only** represent a single nucleotide; "**Xaa**" can **only** represent a single amino acid



IFWO

RAW SEQUENCE LISTING

DATE: 02/26/2007

PATENT APPLICATION: US/10/578,839A

TIME: 14:32:39

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Output Set: N:\CRF4\02262007\J578839A.raw

3 <110> APPLICANT: INJE UNIVERSITY
 5 <120> TITLE OF INVENTION: CANCER CELL TARGETING GENE DELIVERY METHOD
 7 <130> FILE REFERENCE: Q94769
 9 <140> CURRENT APPLICATION NUMBER: US 10/578,839A
 10 <141> CURRENT FILING DATE: 2006-05-10
 12 <150> PRIOR APPLICATION NUMBER: KR 10-2003-0079897
 13 <151> PRIOR FILING DATE: 2003-11-12
 15 <150> PRIOR APPLICATION NUMBER: PCT/KR2004/000545
 16 <151> PRIOR FILING DATE: 2004-03-15
 18 <160> NUMBER OF SEQ ID NOS: 11
 20 <170> SOFTWARE: KopatentIn 1.71
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 36
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Artificial Sequence
 27 <220> FEATURE:
 28 <223> OTHER INFORMATION: Env F primer
 31 <400> SEQUENCE: 1
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 35 <210> SEQ ID NO: 2
 36 <211> LENGTH: 47
 37 <212> TYPE: DNA
 38 <213> ORGANISM: Artificial Sequence
 40 <220> FEATURE:
 41 <223> OTHER INFORMATION: 597LN primer
 44 <400> SEQUENCE: 2
 45 agctggacct ggctgccacc acctccgcta ttttgggtccc attttac 47
 48 <210> SEQ ID NO: 3
 49 <211> LENGTH: 49
 50 <212> TYPE: DNA
 51 <213> ORGANISM: Artificial Sequence
 53 <220> FEATURE:
 54 <223> OTHER INFORMATION: LC597 primer
 57 <400> SEQUENCE: 3
 58 caaccccgcc gcaggtggag gaggcagtga atggactcaa aaatttcaa 49
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 62 <211> LENGTH: 35
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial Sequence
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: Spike R2 primer
 70 <400> SEQUENCE: 4
 71 tgctctagaa ttcttaaagg ttaccttcgt tctct 35

see pg 3-4

**Does Not Comply
Corrected Diskette Needed**

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79 <220> FEATURE:
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83 <400> SEQUENCE: 5
84 ggaggtggtg gcagccaggt ccagctagtg cagtct 36
87 <210> SEQ ID NO: 6
88 <211> LENGTH: 36
89 <212> TYPE: DNA
90 <213> ORGANISM: Artificial Sequence
92 <220> FEATURE:
93 <223> OTHER INFORMATION: ScFvLnkC primer
96 <400> SEQUENCE: 6
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101 <211> LENGTH: 2058
102 <212> TYPE: DNA
103 <213> ORGANISM: Gibbon Ape leukemia virus
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107 <222> LOCATION: (1)..(126)
109 <220> FEATURE:
110 <221> NAME/KEY: misc_feature
111 <222> LOCATION: (127)..(1467)
112 <223> OTHER INFORMATION: surface subunit region
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116 <221> NAME/KEY: misc_feature
117 <222> LOCATION: (1468)..(2025)
118 <223> OTHER INFORMATION: transmembrin domain
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126 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtactg 180
128 tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
130 cccacactta aacctgatgt atgtgccttg gcggctagtc ttgagtcctg ggatatcccg 300
132 ggaaccgatg tctcgtcctc taaacgagtc agacctccgg actcagacta tactgccgct 360
134 tataagcaaa tcacctgggg agccataggg tgcagctacc ctgaggctag gactagaatg 420
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144 ttcacagaca aaggaaaatt atccaaggac tggataacgg gaaaaacctg gggattaaga 720
146 ttctatgtgt ctggacatcc aggcgtacag ttcaccattc gcttaaaaat caccaacatg 780
148 ccagctgttg cagtaggctc tgacctcgtc cttgtggaac aaggacctcc tagaacgtcc 840
150 ctgcgtctcc cactcctctc tcccccaagg gaagcgccac cgccatctct ccccgactct 900
152 aactccacag ccttggcgac tagtgnacaa actcccacgg tgagaaaaac aattgttacc 960
154 ctaaacactc cgctcccccac cacaggcgac agactttttg atcttgtgca gggggccttc 1020

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160 gaccgggtgcc gctggggggac ccaaggaaaag ctcaccctca ctgaggtctc aggacacggg 1200
162 ttgtgcatag gaaaggtgcc ctttaccat cagcatctct gcaatcagac cctatccatc 1260
164 aattcctccg gagaccatca gtatctgctc ccctccaacc atagctggtg ggcttgacgc 1320
166 actggcctca ccccttgccct ctccacctca gtttttaatc agactagaga tttctgtatc 1380
168 cagggtccagc tgattcctcg catctattac tatcctgaag aagttttgtt acaggcctat 1440
170 gacaattctc accccaggac taaaagagag gctgtctcac ttaccctagc tgttttactg 1500
172 ggggtgggaa tcacggcggg aataggctac ggttcaactg ccttaattaa aggacctata 1560
174 gacctccagc aaggcctgac aagcctccag atcgccatag atgctgacct ccggggccctc 1620
176 caagactcag tcagcaagtt agaggactca ctgacttccc tgtccgaggt agtgctccaa 1680
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180 gaagagtgtt gtttttacat agaccactca ggtgcagtac gggactccat gaaaaaactc 1800
182 aaagaaaaac tggataaaag acagtttagag cgccagaaaa gccaaaactg gtatgaagga 1860
184 tggttcaata actccccttg gttcactacc ctgctatcaa ccacgctgg gccctatta 1920
186 ctctccttc tgttgctcat cctcgggcca tgcctcatca ataagttagt tcaattcatc 1980
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190 aacgaaggta acctttaa 2058

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193 <210> SEQ ID NO: 8

194 <211> LENGTH: 786

195 <212> TYPE: DNA

196 <213> ORGANISM: Artificial sequence

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199 <221> NAME/KEY: misc_feature

200 <222> LOCATION: (346)..(390)

201 <223> OTHER INFORMATION: (Gly4Ser)3 linker

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205 <221> NAME/KEY: misc_feature

206 <222> LOCATION: (739)..(777)

207 <223> OTHER INFORMATION: PreS1 Tag

210 <400> SEQUENCE: 8

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215 cctggacaac gccttgagtg gatgggatat tttctcctg gcaacgatga ttttaaatac 180
217 tcccagaagt tccagggacg cgtgacaatc actgcagaca aatccgagag cacagcctac 240
219 atggagctga gcagcctgag atctgaggac acggcggtct attactgtgc aagatcggtg 300
221 aacatggcat actggggcca agggactctg gtcactgtct cttcagggtg aggcggttca 360
223 ggccggaggtg gctctggcgg tggcggatcg gacattgtga tgaccagtc tccagactcc 420
225 ctggctgtgt ctctgggcga gagggccacc atcaactgca agtccagcca gactgtttta 480
227 tacagcagca acaataagaa ctacttagct tggtagcagc agaaaccagg acagcctcct 540
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231 agcgggtctg ggacagattt cactctcacc atcagcagcc tgcaggctga agatgtggca 660
233 gtttattact gtcagcaata ttattcctat ccggtgacgt tcggccaagg gaccaagggtg 720
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240 <210> SEQ ID NO: 9

241 <211> LENGTH: 13

242 <212> TYPE: PRT

243 <213> ORGANISM: PreS1 epitope at C-terminal of Tag-72pS1

*this is not entirely explained**what about locations 1-345, 391-738, 778-786?**they need explanation**what is (are) their source(s)? see item 11 on Error summary sheet**invalid <213> response (see item 10 on Error summary sheet)*

RAW SEQUENCE LISTING

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251 <211> LENGTH: 2871
252 <212> TYPE: DNA
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: ScFv-GaLV Env GP chimeric peptide (FvGEL199) DNA
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264 gggacgagtc tgcaaaataa gaacccccac cagcccatga ccctcacttg gcaggtagtg 180
266 tcccaaactg gagacgttgt ctgggataca aaggcagtc agcccccttg gacttggtgg 240
268 cccacactta aacctgatgt atgtgccttg gcggtagtc ttgagtcctg ggatatcccg 300
270 ggaaccgatg tctcgtcttc taaacgagtc agacctccgg actcagacta tactgccgct 360
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280 ggtggtggca gccagggtcca gctagtgcag tctggggctg aagtgaagaa gcctgggggt 660
282 tcagtgaagg tgcctgcaa ggcttctggc tacaccttca ctgaccatgc aattcactgg 720
284 gtgcgccagg cccctggaca acgccttgag tggatgggat atttttctcc tggcaacgat 780
286 gattttaaat actcccagaa gttccaggga cgcgtgacaa tctactgcaga caaatccgcg 840
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296 cagagtgttt tatacagcag caacaataag aactacttag cttggtacca gcagaaacca 1140
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326 aagctcacc tcactgaggt ctcaggacac gggttgtgca taggaaagg gccccttacc 2040
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330 ctcccccca accatagctg gtgggcttgc agcactggcc tcacccttg cctctccacc 2160
332 tcagttttta atcagactag agatttctgt atccaggctc agctgattcc tcgcatctat 2220
334 tactatcttg aagaagtttt gttacaggcc tatgacaatt ctacccccag gactaaaaga 2280
336 gaggtgtct cacttacct agctgtttta ctgggggttg gaatcacggc gggaatagg 2340

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342 tcaactgactt ccctgtccga ggtagtgtc caaaatagga gaggccttga cttgctgttt 2520
344 ctaaaagaag gtggcctctg tgcggcccta aaggaagagt gctgttttta catagaccac 2580
346 tcaggtgcag tacgggactc catgaaaaaa ctcaaagaaa aactggataa aagacagtta 2640
348 gagcgccaga aaagccaaaa ctggtatgaa ggatggttca ataactcccc ttggttcact 2700
350 accctgctat caaccatcgc tgggccccta ttactcctcc ttctgttgct catcctcggg 2760
352 ccatgcatca tcaataagtt agttcaattc atcaatgata ggataagtgc agttaaatt 2820
354 ctggtcctta gacaaaaata tcaggcccta gagaacgaag gtaaccttta a 2871
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358 <211> LENGTH: 956
359 <212> TYPE: PRT
360 <213> ORGANISM: Artificial Sequence
362 <220> FEATURE:
363 <223> OTHER INFORMATION: ScFv-GaLV Env GP chimeric ligand (FvGEL199)
366 <400> SEQUENCE: 11
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370 Leu Arg His Gln Met Ser Pro Gly Ser Trp Lys Arg Leu Ile Ile Leu
371 20 25 30
373 Leu Ser Cys Val Phe Gly Gly Gly Gly Thr Ser Leu Gln Asn Lys Asn
374 35 40 45
376 Pro His Gln Pro Met Thr Leu Thr Trp Gln Val Leu Ser Gln Thr Gly
377 50 55 60
379 Asp Val Val Trp Asp Thr Lys Ala Val Gln Pro Pro Trp Thr Trp Trp
380 65 70 75 80
382 Pro Thr Leu Lys Pro Asp Val Cys Ala Leu Ala Ala Ser Leu Glu Ser
383 85 90 95
385 Trp Asp Ile Pro Gly Thr Asp Val Ser Ser Ser Lys Arg Val Arg Pro
386 100 105 110
388 Pro Asp Ser Asp Tyr Thr Ala Ala Tyr Lys Gln Ile Thr Trp Gly Ala
389 115 120 125
391 Ile Gly Cys Ser Tyr Pro Arg Ala Arg Thr Arg Met Ala Ser Ser Thr
392 130 135 140
394 Phe Tyr Val Cys Pro Arg Asp Gly Arg Thr Leu Ser Glu Ala Arg Arg
395 145 150 155 160
397 Cys Gly Gly Leu Glu Ser Leu Tyr Cys Lys Glu Trp Asp Cys Glu Thr
398 165 170 175
400 Thr Gly Thr Gly Tyr Trp Leu Ser Lys Ser Ser Lys Asp Leu Ile Thr
401 180 185 190
403 Val Lys Trp Asp Gln Asn Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
404 195 200 205
406 Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val
407 210 215 220
409 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp His Ala Ile His Trp
410 225 230 235 240
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413 245 250 255
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VERIFICATION SUMMARY

DATE: 02/26/2007

PATENT APPLICATION: US/10/578,839A

TIME: 14:32:40

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